Shears, Beverly

From: Devi, Sarvamangala
Sent: Monday, June 10, 2002 7:17 AM
To: Shears, Beverly
Subject: 09/388,090

Good morning Beverly:

Would you please perform a text search for the following claim:

An isolated nucleic acid (DNA) comprising a nucleotide sequence encoding a polypeptide of a Neisseria species, which polypeptide has a molecular weight of about 40 kD to about 55 kD and contains a serine protease motif.

Note: Examples of Neisseria species include Neisseria gonorrh?ea? (gonococc?); Neisseria catarrhalis; Neisseria lactamica; Neisseria ovis; Neisseria lacunata; Neisseria bovis; and Neisseria osloensis.

Please cover all databases, especially Medical, veterinary and agricultural databases; Dissertation Abstracts; Inside Conferences; PASCAL; JICST.

Thank you.

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Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

Devi, S.
09/388090

17jun02 10:11:49 User219783 Session D1832.1

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Set Items Description
--- ----- -----

Key terms w/ term ser protease

Set Items Description
S1 131177 (NUCLEIC OR DEOXYRIBONUCLEIC OR DEOXY(W)RIBONUCLEIC OR DNA) AND NUCLEOTIDE? ?
S2 73131 S1 AND (POLYPROTEIN? ? OR POLYPEPTIDE? ? OR PROTEIN? ? OR -PEPTIDE? ?)
S3 804 S2 AND (NEISSER? OR (NEISSER? OR N)(W)(GONOCOCC? OR GONORR-H? OR CATARRHAL? OR LACTAMIC? OR OVIS OR LACUNATA OR BOVIS OR

S17 309 MOTIF? ?(S)((SERINE OR SER)(W)(PROTEASE? ? OR PROTEINASE? -?))
S18 1 S3 AND S17
>>>No matching display code(s) found in file(s): 65, 113

18/3,AB/1 (Item 1 from file: 348)
DIALOG(R)File 348:EUROPEAN PATENTS
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01270274
Lawsonia intracellularis proteins, and related methods and materials
Lawsonia intracellularis Proteine sowie Methoden und Materialien die diese verwenden
Proteines de Lawsonia intracellularis et procedes et materiaux relatifs a ces proteines
PATENT ASSIGNEE:
Pfizer Products Inc., (2434221), Eastern Point Road, Groton, Connecticut 06340, (US), (Applicant designated States: all)
INVENTOR:
Rosey, Everett Lee, Pfizer Central Research, Eastern Point Road, Groton, Connecticut 06340, (US)
LEGAL REPRESENTATIVE:

Eddowes, Simon et al (87482), Urquhart-Dykes & Lord, 30 Welbeck Street, London W1G 8ER, (GB)
PATENT (CC, No, Kind, Date): EP 1094070 A2 010425 (Basic)
EP 1094070 A3 020109
APPLICATION (CC, No, Date): EP 2000309125 001017;
PRIORITY (CC, No, Date): US 160922 P 991022
DESIGNATED STATES: AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LI; LU; MC; NL; PT; SE
EXTENDED DESIGNATED STATES: AL; LT; LV; MK; RO; SI
INTERNATIONAL PATENT CLASS: C07K-014/205; C12N-015/31

ABSTRACT EP 1094070 A2
Isolated polynucleotide molecules contain a nucleotide sequence that encodes a L. intracellularis HtrA, PonA, HypC, LysS, YcfW, ABC1, or Omp100 protein, a substantial portion of the sequences, or a homologous sequence. Related polypeptides, immunogenic compositions and assays are described.
ABSTRACT WORD COUNT: 40
NOTE:
Figure number on first page: 1

LANGUAGE (Publication,Procedural,Application): English; English; English
FULLTEXT AVAILABILITY:

Available Text	Language	Update	Word Count
CLAIMS A	(English)	200117	864
SPEC A	(English)	200117	25111
Total word count - document A			25975
Total word count - document B			0
Total word count - documents A + B			25975

w/o term Ser protease

Set	Items	Description
S4	71439	(NUCLEIC OR DEOXYRIBONUCLEIC OR DEOXY(W)RIBONUCLEIC OR DNA-)(S)NUCLEOTIDE? ?
S5	32164	S4(S)(POLYPROTEIN? ? OR POLYPEPTIDE? ? OR PROTEIN? ? OR PEPTIDE? ?)
S6	124	S5(S)(NEISSER? OR (NEISSER? OR N)(W)(GONOCOCC? OR GONORRH? OR CATARRHAL? OR LACTAMIC? OR OVIS OR LACUNATA OR BOVIS OR OSLOENSIS))
S8	69	S6(S)ENCOD?
S10	17	S8(S)(ISOLAT? OR ISOL? ?)
S19	17	S10 NOT S18

>>>No matching display code(s) found in file(s): 65, 113

19/3,AB/1 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

11092874 PASCAL No.: 93-0599895
Cloning and characterization of Neisseria meningitidis genes encoding the transferrin-binding proteins Tbp1 and Tbp2
LEGRAIN M; MAZARIN V; IRWIN S W; BOUCHON B; QUENTIN-MILLET M J; JACOBS E; SCHRYVERS A B
Transgene, 67082 Strasbourg, France; Pasteur-Merieux serums vaccins, 69280 Marcy L'Etoile, France
Journal: Gene, 1993, 130 (1) 73-80

Language: English
Genes tbp1 and tbp2, *encoding"** the transferrin-binding *proteins"** Tbp1 and Tbp2, have been *isolated"** from two strains of *Neisseria"** meningitidis. The tbp2 and tbp1 open reading frames are tandemly arranged in the genome with an 87-bp intergenic region, and the *DNA"** region upstream from the tbp2-coding sequence contains domains homologous to Escherichia coli promoter consensus motives. *Nucleotide"** sequence analysis suggests the existence of a Tbp1 precursor carrying an N-terminal signal *peptide"** with a peptidase I cleavage site and of a Tbp2 precursor with N-terminal homology to lipoproteins, including a peptidase II cleavage site. Comparison of the Tbp1 deduced amino acid (aa) sequences from both strains showed about 76% aa homology, while those of Tbp2 revealed only about 47% aa homology

19/3,AB/2 (Item 1 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

12441791 References: 41
TITLE: exl, an exchangeable genetic island in Neisseria meningitidis
AUTHOR(S): Kahler CM (REPRINT); Blum E; Miller YK; Ryan D; Popovic T; Stephens DS
AUTHOR(S) E-MAIL: charlene.kakler@monash.edu.au
CORPORATE SOURCE: Monash Univ, Dept Microbiol, Wellington Rd/Clayton/Vic 3800/Australia/ (REPRINT); Emory Univ, Dept Med, /Atlanta//GA/; Emory Univ, Dept Microbiol & Immunol, /Atlanta//GA/30322; Vet Adm Med Ctr, Res Serv, /Atlanta//GA/30033; Ctr Dis Control & Prevent, /Atlanta//GA/; State Univ W Georgia, /Carrollton//GA/
PUBLICATION TYPE: JOURNAL
PUBLICATION: INFECTION AND IMMUNITY, 2001, V69, N3 (MAR), P1687-1696
GENUINE ARTICLE#: 404GZ
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA
ISSN: 0019-9567
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The genetic structure and evolution of a novel exchangeable meningococcal genomic island was defined for the important human pathogen *Neisseria"** meningitidis, In 125 meningococcal strains tested, one of three unrelated *nucleotide"** sequences, designated exl (exchangeable locus), was found between a gene required for heme utilization, hemO, and col, *encoding"** a putative Escherichia coli collagenase homologue. The 5' boundary of each exl cassette was the stop codon of hemO, whereas the 3' boundary was delineated by a 33-bp repeat containing *neisserial"** uptake sequences located downstream of col. One of the three alternative exl cassettes contained the meningococcal hemoglobin receptor gene, hmbR (exl3), In other meningococcal strains, hmbR was absent from the genome and was replaced by either a *nucleotide"** sequence containing a novel open reading frame, exl2, or a cassette containing exl3. The *proteins"** *encoded"** by exl2 and exl3 had no significant amino acid homology to HmbR but contained six motifs that are also present in the lipoprotein components of the lactoferrin (LbpB), transferrin (TbpB), and hemoglobin-haptoglobin (HpuA) uptake systems. To determine the evolutionary relationships among meningococci carrying hmbR, exl2, or exl3, *isolates"** representing 92 electrophoretic types were examined. hmbR was found throughout the population structure of N. meningitidis (genetic distance, >0.425), whereas exl2 and exl3 were found in clonal groups at genetic

distances of <0.2. The commensal *neisserial"** species were identified as reservoirs for all of the exl cassettes found in meningococci. The structure of these cassettes and their correlation with clonal groups emphasize the extensive gene pool and frequent horizontal *DNA"** transfer events that contribute to the evolution and virulence of N. meningitidis.

19/3,AB/3 (Item 2 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

08050730 References: 16
TITLE: Molecular cloning and expression of NlaIII restriction-modification system in E-coli
AUTHOR(S): Morgan RD; Camp RR; Wilson GG; Xu SY (REPRINT)
CORPORATE SOURCE: NEW ENGLAND BIOLABS INC,32 TOZER RD/BEVERLY//MA/01915 (REPRINT); NEW ENGLAND BIOLABS INC,/BEVERLY//MA/01915; GORDON COLL,DEPT BIOL/WENHAM//MA/01984
PUBLICATION TYPE: JOURNAL
PUBLICATION: GENE, 1996, V183, N1-2 (DEC 12), P215-218
GENUINE ARTICLE#: VZ989
PUBLISHER: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
ISSN: 0378-1119
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The NlaIII restriction enzyme *isolated"** from *Neisseria"** *lactamica"** recognizes the sequence 5'-CATG-3', cleaving after the G to generate a four base 3' overhang. The NlaIII methylase and a portion of the NlaIII endonuclease gene were cloned into E. coli by the methylase selection method, and the remaining portion of the NlaIII endonuclease gene was cloned by inverse PCR. The *nucleotide"** sequence of the endonuclease gene and the methylase gene were determined. The NlaIII endonuclease gene is 693 bp, *encoding"** a *protein"** with predicted molecular weight of 26 487. The NlaIII methylase gene was identical with that previously reported [Labbe, D., Joltke, H.J. and Lau, P.C. (1990) Cloning and characterization of two tandemly arranged *DNA"** methyltransferse genes of *Neisseria"** *lactamica"**: an adenine-specific M.NlaIII and a cytosine-type methylase. Mol. Gen. Genet. 224, 101-110]. The endonuclease and methylase genes overlap by four bases and are transcribed in the same orientation. The endonuclease gene was cloned into an improved T7 vector, and a high level of NlaIII endonuclease expression was achieved in E. coli.

19/3,AB/4 (Item 3 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

07535767 References: 45
TITLE: ANTIGENIC DIVERSITY OF MENINGOCOCCAL OUTER MEMBRANE PROTEIN PORA HAS IMPLICATIONS FOR EPIDEMIOLOGICAL ANALYSIS AND VACCINE DESIGN
AUTHOR(S): FEAVERS IM; FOX AJ; GRAY S; JONES DM; MAIDEN MCJ (Reprint)
CORPORATE SOURCE: NATL INST BIOL STAND & CONTROLS,DIV BACTERIOL,BLANCHE LANE S MIMMS/POTTERS BAR EN6 3QG/HERTS/ENGLAND/ (Reprint); NATL INST BIOL STAND & CONTROLS,DIV BACTERIOL/POTTERS BAR EN6 3QG/HERTS/ENGLAND/; WITHINGTON HOSP,MRU PUBL HLTH LAB/MANCHESTER M20 8LR/LANCS/ENGLAND/
PUBLICATION: CLINICAL AND DIAGNOSTIC LABORATORY IMMUNOLOGY, 1996, V3, N4 (JUL), P444-450
GENUINE ARTICLE#: UV503

ISSN: 1071-412X
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The currently used serological subtyping scheme for the pathogen *Neisseria"** meningitidis is not comprehensive, a proportion of *isolates"** are reported as not subtypeable (NST), and few *isolates"** are fully characterized with two subtypes for each strain. To establish the reasons for this and to assess the effectiveness of *DNA"**-based subtyping schemes, dot blot hybridization and *nucleotide"** sequence analyses were used to characterize the genes *encoding"** antigenic variants of the meningococcal subtyping antigen, the PorA *protein"**. pi total of 233 strains, including 174 serologically NST and 59 partially or completely subtyped meningococcal strains, were surveyed. The NST *isolates"** were chosen to be temporally and geographically representative of NST strains, *isolated"** in England and Wales, and submitted to the Meningococcal Reference Unit in the period 1989 to 1991. The *DNA"**-based analyses demonstrated that all of the strains examined possessed a porA gene. Some of these strains were serologically NST because of a lack of monoclonal antibodies against certain PorA epitopes; in other cases, strains expressed minor variants of known PorA epitopes that did not react with monoclonal antibodies in serological assays. Lack of expression remained a possible explanation for serological typing failure in some cases. These findings have important implications for epidemiological analysis and vaccine design and demonstrate the need for genetic characterization, rather than phenotypic characterization using monoclonal antibodies, for the identification of meningococcal strains.

19/3,AB/5 (Item 4 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

06475536 References: 56
TITLE: CHARACTERIZATION OF THE PILF-PILD PILUS-ASSEMBLY LOCUS OF NEISSERIA GONORRHOEAE
AUTHOR(S): FREITAG NE; SEIFERT HS; KOOMEY M (Reprint)
CORPORATE SOURCE: UNIV MICHIGAN,SCH MED,DEPT MICROBIOL & IMMUNOL/ANN ARBOR//MI/48109 (Reprint); UNIV MICHIGAN,SCH MED,DEPT MICROBIOL & IMMUNOL/ANN ARBOR//MI/48109; NORTHWESTERN UNIV,SCH MED,DEPT MICROBIOL IMMUNOL/CHICAGO//IL/60611
PUBLICATION: MOLECULAR MICROBIOLOGY, 1995, V16, N3 (MAY), P575-586
GENUINE ARTICLE#: RC361
ISSN: 0950-382X
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Expression of Type IV pill by the bacterial pathogen *Neisseria"** *gonorrhoeae"** appears to be essential for colonization of the human host. Several N. gonerrhoeae gene products have been recently identified which bear homology to *proteins"** involved in pilus assembly and *protein"** export in other bacterial systems. We report here the *isolation"** and characterization of transposon insertion mutants in *N"** . *gonorrhoeae"** whose phenotypes indicate that the N. gonerrhoeae pilF and pilD gene products are required for gonoccocal pilus biogenesis. Mutants lacking the pilD gene product, a pre-pilin peptidase, were unable to process the pre-pilin subunit into pilin and thus were nonpiliated, pilF mutants processed pilin but did not assemble the mature subunit. Both classes of mutants released S-pilin, a soluble, truncated form of the pilin subunit previously correlated with defects in pilus assembly. In addition,

mutants containing transposon insertions in pilD or in a downstream gene, orfX, exhibited a severely restricted growth phenotype. Deletion analysis of pilD indicated that the poor growth phenotype observed for the pilD transposon mutants was a result of polar effects of the insertions on orfX expression, orfX *encodes"** a predicted *polypeptide"** of 23 kDa which contains a consensus *nucleotide"**-binding domain and has apparent homologues in Pseudomonas aeruginosa, Pseudomonas putida, Thermus thermophilus, and the eukaryote Caenorhabditis elegans. Although expression of orfX and pilD appears to be transcriptionally coupled, mutants containing transposon insertions in orfX expressed pill. Unlike either pilF or pilD mutants, orfX mutants were also competent for *DNA"** transformation.

19/3,AB/6 (Item 5 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

05954189 References: 32
TITLE: LIPOOLIGOSACCHARIDE BIOSYNTHESIS IN NEISSERIA GONORRHOEAE - CLONING, IDENTIFICATION AND CHARACTERIZATION OF THE ALPHA-1,5 HEPTOSYLTRANSFERASE I GENE (RFAC)
AUTHOR(S): ZHOU DG; LEE NG; APICELLA MA (Reprint)
CORPORATE SOURCE: UNIV IOWA,DEPT MICROBIOL,51 NEWTON RD/IOWA CITY//IA/52242 (Reprint); UNIV IOWA,DEPT MICROBIOL/IOWA CITY//IA/52242
PUBLICATION: MOLECULAR MICROBIOLOGY, 1994, V14, N4 (NOV), P609-618
GENUINE ARTICLE#: PU230
ISSN: 0950-382X
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The identical partial deep-core structure of Hep alpha 1-3Hep alpha 1-5KDO in Salmonella typhimurium LT2 LPS and *Neisseria"** *gonorrhoeae"** LOS enabled us to *isolate"** a *DNA"** fragment from *N"** . *gonorrhoeae"** that was able to complement the alpha 1,5 LOS heptosyltransferase defect in the S. typhimurium rfaC630 (SA1377) mutant. SDS-PAGE analysis confirmed the production of wild-type LPS in the transformant. Subcloning revealed that complementation was due to a 1.2 kb fragment. Sequence analysis revealed a complete open reading frame capable of *encoding"** a 36-37 kDa *peptide"**. In vitro transcription-translation analysis of the 1.2 kb clone confirmed that a 37 kDa *protein"** was *encoded"** by this *DNA"** fragment. The *DNA"** sequence-deduced *protein"** had 36% identity and 58% similarity to S. typhimurium heptosyltransferase (RfaC). Primer extension analysis indicated that transcription of the cloned gene in *N"**. *gonorrhoeae"** strain 1291 begins 144 bp upstream of the start codon at a G *nucleotide"**. An isogenic mutant of *N"**. *gonorrhoeae"** strain 1291 with an m-Tn3 insertion inside the coding sequence expressed a single truncated LOS with a similar molecular mass to S. typhimurium rfaC LPS. We conclude that the 1.2 kb fragment *encodes"** the alpha 1,5 LOS heptosyltransferase I (RfaC) in *N"**. *gonorrhoeae"**. Our studies also provide further evidence that the third KDO residue in S. typhimurium LPS is added after the core synthesis is completed.

19/3,AB/7 (Item 6 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

05607408 References: 51
TITLE: MOLECULAR CLONING AND ANALYSIS OF GENES FOR SIALIC ACID SYNTHESIS IN NEISSERIA MENINGITIDIS GROUP B AND PURIFICATION OF THE MENINGOCOCCAL CMP-NEUNAC SYNTHETASE ENZYME
AUTHOR(S): GANGULI S; ZAPATA G; WALLIS T; REID C; BOULNOIS G; VANN WF; ROBERTS IS (Reprint)
CORPORATE SOURCE: UNIV LEICESTER,DEPT MICROBIOL/LEICESTER LE1 7RH//ENGLAND/ (Reprint); UNIV LEICESTER,DEPT MICROBIOL/LEICESTER LE1 7RH//ENGLAND/; US FDA,CTR BIOL EVALUAT & RES,BACTERIAL POLYSACCHARIDES LAB/BETHESDA//MD/20892
PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N15 (AUG), P4583-4589
GENUINE ARTICLE#: NY398
ISSN: 0021-9193
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The gene *encoding"** for the CMP-NeuNAc synthetase enzyme of *Neisseria"** meningitidis group B was cloned by complementation of a mutant of Escherichia coli defective for this enzyme. The gene (neuA) was *isolated"** on a 4.1-kb fragment of meningococcal chromosomal *DNA"**. Determination of the *nucleotide"** sequence of this fragment revealed the presence of three genes, termed neuA, neuB, and neuC, organized in a single operon. The presence of a truncated ctr A gene at one end of the cloned *DNA"** and a truncated gene *encoding"** for the meningococcal sialyltransferase at the other confirmed that the cloned *DNA"** corresponded to region A and part of region C of the meningococcal capsule gene cluster. The predicted amino acid sequence of the meningococcal NeuA *protein"** was 57% homologous to that of NeuA, the CMP-NeuNAc synthetase *encoded"** by E. coli K1. The predicted molecular mass of meningococcal NeuA *protein"** was 24.8 kDa, which was 6 kDa larger than that formerly predicted (U. Edwards and M. Frosch, FEMS Microbiol. Lett, 96:161-166, 1992). Purification of the recombinant meningococcal NeuA *protein"** together with determination of the N-terminal amino acid sequence confirmed that this 24.8-kDa *protein"** was indeed the meningococcal CMP-NeuNAc synthetase. The predicted amino acid sequences of the two other *encoded"** *proteins"** were homologous to those of the NeuC and NeuB *proteins"** of E. coli K1, two *proteins"** involved in the synthesis of NeuNAc. These results indicate that common steps exist in the biosynthesis of NeuNAc in these two microorganisms.

19/3,AB/8 (Item 7 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

05314950 References: 61
TITLE: ISOLATION AND CHARACTERIZATION OF A GENE INVOLVED IN HEMAGGLUTINATION BY AN AVIAN PATHOGENIC ESCHERICHIA COLI STRAIN
AUTHOR(S): PROVENCE DL; CURTISS R
CORPORATE SOURCE: ST LOUIS UNIV,SCH MED,DEPT CELL BIOL & PHYSIOL/ST LOUIS//MO/63110 (Reprint); WASHINGTON UNIV,DEPT BIOL/ST LOUIS//MO/63130
PUBLICATION: INFECTION AND IMMUNITY, 1994, V62, N4 (APR), P1369-1380
GENUINE ARTICLE#: NC074
ISSN: 0019-9567
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: In this article, we report the *isolation"** and characterization of a gene that may be important in the adherence of avian pathogenic Escherichia coli to the avian respiratory tract. The E. coil strain HB101,

which is unable to agglutinate chicken erythrocytes, was transduced with cosmid libraries from the avian pathogenic E. coil strain (chi)7122. Enrichment of transductants that could agglutinate thicken erythrocytes yielded 19 colonies. These *isolates"** contained cosmids that encompassed four nonoverlapping regions of the E. coil chromosome. Only one group of cosmids, represented by pYA3104, would cause E. coli CC118 to agglutinate chicken erythrocytes. A IO-kh fragment of this cosmid was subcloned in pACYC184. Transposon mutagenesis of this fragment,vith Tn5seql indicated that a contiguous 4.4-kb region of cloned *DNA"** was required for hemagglutination. In vitro transcription/translation assays indicated that this 4.4-k6 region of *DNA"** *encoded"** one *protein"** of approximately 140 kDa. The *nucleotide"** sequence of this region was determined and found to *encode"** one open reading frame of 4,134 *nucleotides"** that would *encode"** a *protein"** of 1,377 amino acids with a deduced molecular weight of 148,226. This gene confers on E. coil K-12 a temperature-sensitive hemagglutination phenotype that is best expressed when cells are grown at 26 degrees C, and we have designated this gene tsh and the deduced gene product Tsh. Insertional mutagenesis of the chromosomal tsh gene in (chi)7122 had no effect on hemagglutination titers. The deduced *protein"** was found to contain significant homology to the Haemophilus influenzae and *Neisseria"** *gonorrhoeae"** immunoglobulin Al proteases. These data indicate that (i) a single gene *isolated"** from the avian pathogenic E. coli strain (chi)7122 will confer on E. coli K-12 a hemagglutination-positive phenotype, (ii) (chi)7122 contains at least two distinct mechanisms to allow hemagglutination to occur, and (iii) the hemagglutinin Tsh has homology with a class of *proteins"** previously not known to exist in E. coil.

19/3,AB/9 (Item 8 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

04797803 References: 36
TITLE: CLONING AND CHARACTERIZATION OF NEISSERIA-MENINGITIDIS GENES ENCODING THE TRANSFERRIN-BINDING PROTEINS TBP1 AND TBP2
AUTHOR(S): LEGRAIN M; MAZARIN V; IRWIN SW; BOUCHON B; QUENTINMILLET MJ; JACOBS E; SCHRYVERS AB
CORPORATE SOURCE: TRANSGENE SA,11 RUE MOLSHEIM/F-67082 STRASBOURG//FRANCE/ (Reprint); UNIV CALGARY,DEPT MICROBIOL & INFECT DIS/CALGARY T2N 4N1/AB/CANADA/
PUBLICATION: GENE, 1993, V130, N1 (AUG 16), P73-80
GENUINE ARTICLE#: LT636
ISSN: 0378-1119
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Genes tbp1 and tbp2, *encoding"** the transferrin-binding *proteins"** Tbp1 and Tbp2, have been *isolated"** from two strains of *Neisseria"** meningitidis. The tbp2 and tbp1 open reading frames are tandemly arranged in the genome with an 87-bp intergenic region, and the *DNA"** region upstream from the tbp2-coding sequence contains domains homologous to Escherichia coli promoter consensus motives. *Nucleotide"** sequence analysis suggests the existence of a Tbp1 precursor carrying an N-terminal signal *peptide"** with a peptidase I cleavage site and of a Tbp2 precursor with N-terminal homology to lipoproteins, including a peptidase II cleavage site. Comparison of the Tbp1 deduced amino acid (aa) sequences from both strains showed about 76% aa homology, while those of Tbp2 revealed only about 47% aa homology. These comparisons should be

extended to other *Neisseria"** strains in order to evaluate further this genetic divergence further.

19/3,AB/10 (Item 9 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

03596664 References: 40
TITLE: SEQUENCE ANALYSIS AND COMPLEMENTATION STUDIES OF THE ARGJ GENE ENCODING ORNITHINE ACETYLTRANSFERASE FROM NEISSERIA-GONORRHOEAE
AUTHOR(S): MARTIN PR; MULKS MH (Reprint)
CORPORATE SOURCE: MICHIGAN STATE UNIV,DEPT MICROBIOL & PUBL HLTH/E LANSING//MI/48824 (Reprint); MICHIGAN STATE UNIV,DEPT MICROBIOL & PUBL HLTH/E LANSING//MI/48824
PUBLICATION: JOURNAL OF BACTERIOLOGY, 1992, V174, N8 (APR), P2694-2701
GENUINE ARTICLE#: HM899
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Clinical *isolates"** of *Neisseria"** *gonorrhoeae"** frequently are deficient in arginine biosynthesis. These auxotrophs often have defects in the fifth step of the arginine biosynthetic pathway, the conversion of acetylornithine to ornithine. This reaction is catalyzed by the enzyme ornithine acetyltransferase, which is product of the argJ gene. We have cloned and sequenced the gonococcal argJ gene and found that it contains an open reading frame of 1,218 *nucleotides"** and *encodes"** a *peptide"** with a deduced M(r) of 42,879. This predicted size was supported by minicell analysis. This gene was capable of complementing both Escherichia coli argE and argA mutations and of transforming an ArgJ- strain of *N"**. *gonorrhoeae"** to Arg+. Southern blots were able to detect bands that specifically hybridized to the gonococcal argJ gene in genomic *DNA"** from Pseudomonas aeruginosa but not E. coli, a result that reflects the divergent nature of the arginine biosynthetic pathway in these organisms.

19/3,AB/11 (Item 10 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

03474473 References: 33
TITLE: ROLE OF HORIZONTAL GENETIC EXCHANGE IN THE ANTIGENIC VARIATION OF THE CLASS-1 OUTER MEMBRANE PROTEIN OF NEISSERIA-MENINGITIDIS
AUTHOR(S): FEAVERS IM; HEATH AB; BYGRAVES JA; MAIDEN MCJ
CORPORATE SOURCE: NATL INST BIOL STAND & CONTROLS,DIV BACTERIOL,BLANCHE LANE/POTTERS BAR EN6 3QG/HERTS/ENGLAND/ (Reprint); NATL INST BIOL STAND & CONTROLS,DIV INFORMAT/POTTERS BAR EN6 3QG/HERTS/ENGLAND/
PUBLICATION: MOLECULAR MICROBIOLOGY, 1992, V6, N4 (FEB), P489-495
GENUINE ARTICLE#: HE853
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The *nucleotide"** sequences of the genes *encoding"** the class 1 outer membrane *protein"** of *Neisseria"** meningitidis (PorA) from 15 meningococcal *isolates"** have been examined. These strains, *isolated"** over a number of years, represented a variety of serological types, clonal groups, and geographical locations. Analysis of the aligned *nucleotide"** sequences showed that the known serological relationships between these *proteins"** were not necessarily reflected throughout the *nucleotide"**

sequences of their genes. The uneven distribution of base substitutions, revealed by a comparison of the informative bases, suggested that these genes possessed a mosaic structure. This structure probably resulted from the horizontal transfer of *DNA"** between strains and would have contributed to both the generation and the spread of novel antigenic variants of the *protein"**. In addition, the *nucleotide"** differences between porA genes from different strains were not consistent with the *nucleotide"** sequence divergence of the whole chromosome, as indicated by pulsed-field gel electrophoresis (PFGE) fingerprinting techniques: some strains with divergent PFGE fingerprints shared porA genes with extensive regions of *nucleotide"** sequence identity and, conversely, some strains with similar chromosome structures possessed porA genes with different *nucleotide"** sequences and serological properties. This suggested that entire genes had been exchanged between strains. Given that the meningococcal class 1 OMP is a major component in novel vaccines, some of which are currently undergoing field trials, the potential of horizontal genetic exchange to generate antigenic diversity has implications for the design of such vaccines.

19/3,AB/12 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0258656 DBA Accession No.: 2000-13146 PATENT
Neisseria meningitidis serogroup-B antigen - vector-mediated gene transfer and expression in host cell, antibody, agonist, antagonist and DNA primer for recombinant vaccine
AUTHOR: Thonnard J
CORPORATE SOURCE: Rixensart, Belgium.
PATENT ASSIGNEE: SK-Beecham 2000
PATENT NUMBER: WO 200047743 PATENT DATE: 20000817 WPI ACCESSION NO.: 2000-506096 (2045)
PRIORITY APPLIC. NO.: GB 992937 APPLIC. DATE: 19990210
NATIONAL APPLIC. NO.: WO 2000EP888 APPLIC. DATE: 20000204
LANGUAGE: English
ABSTRACT: An *isolated"** *protein"** (164 amino acids) or a *protein"** with at least 85% identity is new. Also claimed are: an immunogenic fragment of the *protein"** with the same activity; a *polynucleotide"** (495 bp) *encoding"** the *protein"**; an expression vector; a vaccine composition containing the *protein"** or *polynucleotide"** and a carrier; an antibody; and a therapeutic composition useful in treating *Neisseria"** meningitidis infection. Also disclosed are: a diagnostic kit; *DNA"** primers; screening for agonists or antagonists; agonists and antagonists; modified host cells capable of producing non-live membrane-based bleb vectors; preparation of host cells and bacterial blebs; and computer-based methods for performing homology identification. The *protein"** may be identified within a biological sample from an animal in order to diagnose a N. meningitidis infection. The *Protein"** and *polynucleotide"** may be used for the preparation of a medicament for use in generating an immune response in an animal. The therapeutic composition is useful in a composition for treating humans with N. meningitidis infection. (79pp)

19/3,AB/13 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0258602 DBA Accession No.: 2000-13092 PATENT
Neisseria meningitidis BASBO47, BASBO54, BASBO68, and BASBO69 proteins, useful for treating N. meningitidis infections, bacteremia, and meningitis - polynucleotide and protein useful for treating disease
AUTHOR: Ruelle J L
CORPORATE SOURCE: Rixensart, Belgium.
PATENT ASSIGNEE: SK-Beecham 2000
PATENT NUMBER: WO 200043519 PATENT DATE: 20000727 WPI ACCESSION NO.: 2000-505839 (2045)
PRIORITY APPLIC. NO.: GB 993535 APPLIC. DATE: 19990216
NATIONAL APPLIC. NO.: WO 2000EP428 APPLIC. DATE: 20000119
LANGUAGE: English
ABSTRACT: A new *isolated"** *protein"** is claimed. It contains an amino acid sequence which has at least 85% identity to a disclosed residue *Neisseria"** meningitidis BASBO47, BASBO54, BASBO68, and BASBO69 amino acid sequence (I-IV). Also claimed are: an *isolated"** *protein"** having any of (I-IV); an *isolated"** *polynucleotide"** containing a *nucleotide"** sequence *encoding"** a *protein"** that has at least 85% identity to any of (I-IV); an *isolated"** *polynucleotide"** which contains a *nucleotide"** sequence which has at least 85% identity to the disclosed bp *DNA"** sequence (V-VIII); an *isolated"** *polynucleotide"** that contains any of (V-VIII); an expression vector containing an *isolated"** *polynucleotide"**; a host cell containing the expression vector; a process for producing a *protein"**; a process for expressing a *polynucleotide"**; a vaccine composition containing the novel *peptide"**; an antibody immunospecific for novel *peptide"** ; diagnosing a *Neisseria"** meningitidis infection; and a therapeutic composition useful in treating *Neisseria"** meningitidis disease. The *polynucleotide"** and *protein"** can be used in vaccine compositions. The antibodies can be used in composition for treating *Neisseria"** meningitidis disease. (103pp)

19/3,AB/14 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0258174 DBA Accession No.: 2000-12664 PATENT
Antigenic BASB058 polypeptides from Neisseria meningitidis and the nucleic acids that encode them, useful for vaccinating against bacteria and meningitis - involving vector-mediated gene transfer for expression in host cell
AUTHOR: Thonnard J
CORPORATE SOURCE: Rixensart, Belgium.
PATENT ASSIGNEE: SK-Beecham-Biol. 2000
PATENT NUMBER: WO 200044890 PATENT DATE: 20000803 WPI ACCESSION NO.: 2000-491239 (2043)
PRIORITY APPLIC. NO.: GB 992084 APPLIC. DATE: 19990129
NATIONAL APPLIC. NO.: WO 2000EP560 APPLIC. DATE: 20000125
LANGUAGE: English
ABSTRACT: BASB058 antigenic *proteins"** (I) from *Neisseria"** meningitidis and the *nucleic"** acids (II) that *encode"** them, are claimed. Also claimed are: an *isolated"** *protein"** (I); an immunogenic fragment of (I); an *isolated"** *polynucleotide"** (II); an expression vector or recombinant live microorganism; a process for expressing (II), comprising transforming and culturing a host cell; an

antibody specific for (I); and a method of diagnosing a N. meningitidis infection. (I) and (II) may be used according to standard methods to produce vaccine compositions which may used to vaccinate against (i.e. generate an immune response against) N. meningitidis. The vaccine compositions preferably further contain at least 1 other N. meningitidis antigen. Compositions comprising antibodies specific for (I) may be used to treat N. meningitidis infections in humans. N. meningitidis is implicated in a number of invasive bacterial disease processes such as bacteremia and meningitis. The new *proteins"** and *nucleic"** acids may be used to vaccinate patients against infections which may otherwise be resistant. (75pp)

19/3,AB/15 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0252760 DBA Accession No.: 2000-07250 PATENT
Neisseria meningitidis NMASP polypeptide, nucleotide sequences and antibodies, useful in vaccines against infection - method is used to induce an immune response to Neisseria meningitidis and Neisseria meningitidis NMASP polypeptide and a NMASP-derived polypeptide in animals
AUTHOR: Jackson W J; Harris A M
CORPORATE SOURCE: Gaithersburg, MD, USA
PATENT ASSIGNEE: Antex-Biologics 2000
PATENT NUMBER: WO 200012535 PATENT DATE: 20000309 WPI ACCESSION NO.: 2000-256581 (2022)
PRIORITY APPLIC. NO.: US 98685 APPLIC. DATE: 19980901
NATIONAL APPLIC. NO.: WO 99US19663 APPLIC. DATE: 19990901
LANGUAGE: English
ABSTRACT: *Neisseria"** meningitidis NMASP *protein"** of mol.wt. 40,000-55,000 (SDS-PAGE) is claimed. Also claimed are: a *peptide"** fragment of NMASP; an *isolated"** antibody that binds NMASP; an antigenic composition (comprises one or more adjuvants) comprising NMASP; an *isolated"** *DNA"** comprising a *nucleotide"** sequence *encoding"** NMASP; an *isolated"** *DNA"** sequence having a 153 base pair sequence; an *isolated"** *DNA"** which comprises a *nucleotide"** sequence that hybridizes to a disclosed sequence; plasmid pNmAH116 obtainable from Escherichia coli; a method (A) for assaying for an agent that interacts with NMASP; an antagonist which inhibits the activity of NMASP; and a method for identifying a compound which interacts with and inhibitor or activate of NMASP. NMASP can be used in a method to produce an immune response in an animal. The sequence and antibody are useful for protection against N. meningitidis, also may be used as ligands to detect antibodies elicited in response to N. meningitidis infection. Antibody generated against the NMASP *polypeptide"** in an animal host will exhibit bactericidal or opsonic activity against many N. meningitidis strains. (75pp)

19/3,AB/16 (Item 5 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0252684 DBA Accession No.: 2000-07174 PATENT
Non-cytosolic NGSP polypepetide and polynucleotide sequence from Neisseria useful for diagnosis, prevention or treatment of Neisseria infections

- method is used for inducing an immune response to Neisseria and Neisseria NGSP polypeptide and a NGSP-derived polypeptide in animal
AUTHOR: Jackson W J; Harris A M
CORPORATE SOURCE: Gaithersburg, MD, USA.
PATENT ASSIGNEE: Antex-Biologics 2000
PATENT NUMBER: WO 200012133 PATENT DATE: 20000309 WPI ACCESSION NO.: 2000-237782 (2020)
PRIORITY APPLIC. NO.: US 98685 APPLIC. DATE: 19980901
NATIONAL APPLIC. NO.: WO 99US20070 APPLIC. DATE: 19990901
LANGUAGE: English
ABSTRACT: *Isolated"** NGSP *protein"** (I) of *Neisseria"** spp. having a mol.wt. of 40,000-55,000 (from *Neisseria"** *ovis"**, *Neisseria"** *osloensis"**, *Neisseria"** *bovis"**, *Neisseria"** *gonorrhoeae"** or *Neisseria"** *lacunata"**) is claimed. (I) is a subunit of a non-cytosolic *protein"** located in the bacterial envelope. Also claimed are: a *peptide"** fragment (II) of (I); an antibody (III) that binds (I); an antigenic composition containing (I) or (II); a pharmaceutical composition of (III); an *isolated"** *DNA"** (IV) comprising a *nucleotide"** sequence *encoding"** (I) or (II); an *isolated"** *DNA"** comprising a sequence which hybridizes to (IV); plasmid pTLZ-NgHtrA number 2 from Escherichia coli JM109; a (I)-antagonist which inhibits (I) activity; a method for identifying compounds which inhibit (I) activity to permit interaction between (A) and (I); and a method for assaying for an agent that interacts with (I) which involves washing the cells and detecting any marker associated with the cells. (I) and (II) can be used to immunize an animal, and also as a ligand to detect antibodies elicited in response to *Neisseria"** infections or as an antigen to induce *Neisseria"** -specific antibodies. (68pp)

19/3,AB/17 (Item 6 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0248452 DBA Accession No.: 2000-02942 PATENT
New polypeptide from Neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal - diagnosis, prophylaxis, therapy, gene therapy, recombinant vaccine and nucleic acid vaccine
AUTHOR: Ruelle J L
CORPORATE SOURCE: Rixensart, Belgium.
PATENT ASSIGNEE: SK-Beecham-Biol. 1999
PATENT NUMBER: WO 9958683 PATENT DATE: 19991118 WPI ACCESSION NO.: 2000-053103 (2004)
PRIORITY APPLIC. NO.: GB 9810276 APPLIC. DATE: 19980513
NATIONAL APPLIC. NO.: WO 99EP3255 APPLIC. DATE: 19990507
LANGUAGE: English
ABSTRACT: An *isolated"** *protein"** (I), BASB029 from *Neisseria"** meningitidis comprises 594 and 591 amino acids (*protein"** sequences disclosed). Also claimed are: a *protein"** 85% or 95% identical to (I); an immunogenic fragment of (I) with the same immunogenic activity as (I); an *isolated"** *polynucleotide"** (II) *encoding"** (I) and having a sequence of 1,785 and 1,776 bp; a *polynucleotide"** (III) having a sequence complementary to (II); a *polynucleotide"** (IV) 85% identical to (II) or its complement; an expression vector or recombinant live microorganism comprising (II), (III) or (IV); a host cell containing the vector or a subcellular fraction of a membrane of a

host cell expressing (I); producing (I) by culturing the transformed host cell under conditions and recovering (I) from the culture medium; expressing (II), (III) or (IV) by transforming host cells and growing them under conditions suited to expression; a recombinant vaccine containing (I); a *nucleic"** acid vaccine containing (II), (III) or (IV); and an antibody immunospecific for (I) or the immunological fragment. (74pp)

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